

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Baker, Joffre
Chien, Kenneth
King, Kathleen
Pennica, Diane
Wood, William

(ii) TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: patin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 05-AUG-1994
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/233609
(B) FILING DATE: 25-APR-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Hasak, Janet E.
(B) REGISTRATION NUMBER: 28,616
(C) REFERENCE/DOCKET NUMBER: 894P1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-1896
(B) TELEFAX: 415/952-9881
(C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1352 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5 GGATAAGCCT GGGGCCAGCA TGAGCCAGAG GGAGGGAAGT CTGGAAGACC 50
10 ACCAGACTGA CTCCTCAATC TCATTCCTAC CCCATTTGGA GGCCAAGATC 100
CGCCAGACAC ACAACCTTGC CCGCCTCCTG ACCAAATATG CAGAACAACCT 150
15 TCTGGAGGAA TACGTGCAGC AACAGGGAGA GCCCTTTGGG CTGCCGGGGCT 200
TCTCACCACC GCGGCTGCCG CTGGCCGGCC TGAGTGGCCC GGCTCCGAGC 250
20 CATGCAGGGC TACCGGTGTC CGAGCGGCTG CGGCAGGATG CAGCCGCCCT 300
GAGTGTGCTG CCCGCGCTGT TGGATGCCGT CCGCCGCCGC CAGGCGGAGC 350
25 TGAACCCGCG CGCCCCGCGC CTGCTGCGGA GCCTGGAGGA CGCAGCCCGC 400
CAGGTTCGGG CCCTGGGCGC CGCGGTGGAG ACAGTGCTGG CCGCGCTGGG 450
30 CGCTGCAGCC CGCGGGCCCC GGCCAGAGCC CGTCACCGTC GCCACCCTCT 500
35 TCACGGCCAA CAGCACTGCA GGCATCTTCT CAGCCAAGGT GCTGGGGTTC 550
CACGTGTGCG GCCTCTATGG CGAGTGGGTG AGCCGCACAG AGGGCGACCT 600
40 GGGCCAGCTG GTGCCAGGGG GCGTCGCCTG AGAGTGAATA CTTTTTCTTG 650
TAAGCTCGCT CTGTCTCGCC TCTTTGGCTT CAAATTTTCT GTCTCTCCAT 700
CTGTGTCCTG TGTGTTCTTG GGCTGTCCCT ATCTTTCTGC ATTTGTGTGG 750
50 TCTCTCTCTT CTGCTCTCCT CTCTGCAGGG AGCTTCTTTT TTCCAACAGT 800
TTCTCGTTTT GTCTCTCTCC AGTCTTGAAC ACTTTTGTCT CCGAGAGGTC 850

TCTTTTTGTT TCCTTGTCTC TTGGTTCTTT CTTTGCTTGC TTGCTTGCTT 900

5 GCTTGCTTGT TGTTGAGACA GGGTCTCACC ATATAGCTCT GGATGGCCTG 950

GAACTTGCTA TGTAGGCCAG GCTGGCCTCC AGCTCATAGA GATCCACTTG 1000

10 CCTCCGACTC CCAATTTCCC CATCTGTCTC CCTGTGATCC ATATGGGTAT 1050

15 GTGTAACCCT TACTTTGTCT CATGGAGGTG ACAATTTTTC TCCCTTCAGT 1100

TTCTTTGTTC TTTACTGACC AGAAAAGTGC CTAATTGTCC CCTGGTGGCA 1150

20 AGGCCATTCA CCTTAGGACC TTCCCACCAG TTCCTTTGTA GGCAAATCCC 1200

TCCCCCTTTG AGGTCCTTCC CTTTCATACC GCCCTAGGCT GGTC AATGGA 1250

25 GAGAGAAAGG CAGAAAAACA TCTTTAAAGA GTTTTATTTG AGAATAAATT 1300

30 AATTTTGTGA AATAAAATGT TTAACAATAA AACTAAACTT TTATGAAAAA 1350

AA 1352

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1352 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCTATTCGGA CCCCGGTCGT ACTCGGTCTC CCTCCCTTCA GACCTTCTGG 50

50 TGGTCTGACT GAGGAGTTAG AGTAAGGATG GGGTAAACCT CCGGTTCTAG 100

GCGGTCTGTG TGTTGGAACG GCGGAGGAC TGGTTTATAC GTCTTGTTGA 150

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AGACCTCCTT ATGCACGTCG TTGTCCCTCT CGGGAAACCC GACGGCCCGA 200
AGAGTGGTGG CGCCGACGGC GACCGGCCGG ACTCACCGGG CCGAGGCTCG 250
GTACGTCCCG ATGGCCACAG GCTCGCCGAC GCCGTCCTAC GTCGGCGGGA 300
CTCACACGAC GGGCGCGACA ACCTACGGCA GGC GGCGGCG GTCCGCCTCG 350
ACTTGGGCGC GCGGGGCGCG GACGACGCCT CGGACCTCCT GCGTCGGGCG 400
GTCCAAGCCC GGGACCCGCG GCGCCACCTC TGTCACGACC GGC GCGACCC 450
GCGACGTCGG GCGCCCGGGC CCGGTCTCGG GCAGTGGCAG CCGTGGGAGA 500
AGTGCCGGTT GTCGTGACGT CCGTAGAAGA GTCGGTTCCA CGACCCCAAG 550
GTGCACACGC CGGAGATACC GCTCACCCAC TCGGCGTGTC TCCCGCTGGA 600
CCCGGTCGAC CACGGTCCCC CGCAGCGGAC TCTCACTTAT GAAAAAGAAC 650
ATTCGAGCGA GACAGAGCGG AGAAACCGAA GTTTAAAAGA CAGAGAGGTA 700
GACACAGGAC ACACAAGAAC CCGACAGGGA TAGAAAGACG TAAACACACC 750
AGAGAGAGAA GACGAGAGGA GAGACGTCCC TCGAAGAAAA AAGGTTGTCA 800
AAGAGCAAAA CAGAGAGAGG TCAGAACTTG TGAAACAGA GGCTCTCCAG 850
AGAAAAACAA AGGAACAGAG AACCAAGAAA GAAACGAACG AACGAACGAA 900
CGAACGAACA ACAACTCTGT CCCAGAGTGG TATATCGAGA CCTACCGGAC 950
CTTGAACGAT ACATCCGGTC CGACCGGAGG TCGAGTATCT CTAGGTGAAC 1000
GGAGGCTGAG GGTAAAGGG GTAGACAGAG GGACACTAGG TATACCCATA 1050

CACATTGGGA ATGAAACAGA GTACCTCCAC TGTAAAAAG AGGGAAGTCA 1100

AAGAAACAAG AAATGACTGG TCTTTTCACG GATGAACAGG GGACCACCGT 1150

TCCGGTAAGT GGAATCCTGG AAGGGTGGTC AAGGAAACAT CCGTTTAGGG 1200

AGGGGGAAAC TCCAGGAAGG GAAAGTATGG CGGGATCCGA CCAGTTACCT 1250

CTCTCTTTCC GTCTTTTTGT AGAAATTCT CAAAATAAAC TCTTATTAA 1300

TTAAAAACAT TTATTTTACA AATTGTTATT TTGATTGAA AATACTTTTT 1350

TT 1352

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ser	Gln	Arg	Glu	Gly	Ser	Leu	Glu	Asp	His	Gln	Thr	Asp	Ser
1				5				10						15
Ser	Ile	Ser	Phe	Leu	Pro	His	Leu	Glu	Ala	Lys	Ile	Arg	Gln	Thr
				20				25						30
His	Asn	Leu	Ala	Arg	Leu	Leu	Thr	Lys	Tyr	Ala	Glu	Gln	Leu	Leu
				35				40						45
Glu	Glu	Tyr	Val	Gln	Gln	Gln	Gly	Glu	Pro	Phe	Gly	Leu	Pro	Gly
				50				55						60
Phe	Ser	Pro	Pro	Arg	Leu	Pro	Leu	Ala	Gly	Leu	Ser	Gly	Pro	Ala
				65				70						75
Pro	Ser	His	Ala	Gly	Leu	Pro	Val	Ser	Glu	Arg	Leu	Arg	Gln	Asp
				80				85						90
Ala	Ala	Ala	Leu	Ser	Val	Leu	Pro	Ala	Leu	Leu	Asp	Ala	Val	Arg
				95				100						105
Arg	Arg	Gln	Ala	Glu	Leu	Asn	Pro	Arg	Ala	Pro	Arg	Leu	Leu	Arg
				110				115						120

Ser Leu Glu Asp Ala Ala Arg Gln Val Arg Ala Leu Gly Ala Ala
125 130 135

Val Glu Thr Val Leu Ala Ala Leu Gly Ala Ala Ala Arg Gly Pro
140 145 150

Gly Pro Glu Pro Val Thr Val Ala Thr Leu Phe Thr Ala Asn Ser
155 160 165

Thr Ala Gly Ile Phe Ser Ala Lys Val Leu Gly Phe His Val Cys
170 175 180

Gly Leu Tyr Gly Glu Trp Val Ser Arg Thr Glu Gly Asp Leu Gly
185 190 195

Gln Leu Val Pro Gly Gly Val Ala
200 203

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Phe Thr Glu His Ser Pro Leu Thr Pro His Arg Arg Asp
1 5 10 15

Leu Cys Ser Arg Ser Ile Trp Leu Ala Arg Lys Ile Arg Ser Asp
20 25 30

Leu Thr Ala Leu Thr Glu Ser Tyr Val Lys His Gln Gly Leu Asn
35 40 45

Lys Asn Ile Asn Leu Asp Ser Ala Asp Gly Met Pro Val Ala Ser
50 55 60

Thr Asp Gln Trp Ser Glu Leu Thr Glu Ala Glu Arg Leu Gln Glu
65 70 75

Asn Leu Gln Ala Tyr Arg Thr Phe His Val Leu Leu Ala Arg Leu
80 85 90

Leu Glu Asp Gln Gln Val His Phe Thr Pro Thr Glu Gly Asp Phe
95 100 105

His Gln Ala Ile His Thr Leu Leu Leu Gln Val Ala Ala Phe Ala
110 115 120

Tyr Gln Ile Glu Glu Leu Met Ile Leu Leu Glu Tyr Lys Ile Pro
125 130 135

Arg Asn Glu Ala Asp Gly Met Pro Ile Asn Val Gly Asp Gly Gly
140 145 150
5 Leu Phe Glu Lys Lys Leu Trp Gly Leu Lys Val Leu Gln Glu Leu
155 160 165
Ser Gln Trp Thr Val Arg Ser Ile His Asp Leu Arg Phe Ile Ser
170 175 180
10 Ser His Gln Thr Gly Ile Pro Ala Arg Gly Ser His Tyr Ile Ala
185 190 195
Asn Asn Lys Lys Met
200

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGCCGCGA GCTCGAATTC TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 50

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGAAGGGAG CCGGGATCAG CCAGGGGCCA GCATGAGCCG GAGGGAGGGA 50

45 AGTCTGGAAG ACCCCCAGAC TGATTCCTCA GTCTCACTTC TTCCCCACTT 100

GGAGGCCAAG ATCCGTCAGA CACACAGCCT TGCGCACCTC CTCACCAAAT 150

50 ACGCTGAGCA GCTGCTCCAG GAATATGTGC AGCTCCAGGG AGACCCCTTC 200

GGGCTGCCCA GCTTCTCGCC GCCGCGGCTG CCGGTGGCCG GCCTGAGCGC 250

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CCCGGCTCCG AGCCACGCGG GGCTGCCAGT GCACGAGCGG CTGCGGCTGG 300

5 ACGCGGCGGC GCTGGCCGCG CTGCCCCCGC TGCTGGACGC AGTGTGTCGC 350

CGCCAGGCCG AGCTGAACCC GCGCGCGCCG CGCCTGCTGC GCCGCCTGGA 400

10 GGACGCGGCG CGCCAGGCCC GGGCCCTGGG CGCCGCCGTG GAGGCCTTGC 450

15 TGGCCGCGCT GGGCGCCGCC AACCGCGGGC CCCGGGCCGA GCCCCCGGCC 500

GCCACCGCCT CAGCCGCCTC CGCCACCGGG GTCTTCCCCG CCAAGGTGCT 550

20 GGGGCTCCGC GTTTGCGGCC TCTACCGCGA GTGGCTGAGC CGCACCGAGG 600

GCGACCTGGG CCAGCTGCTG CCCGGGGGCT CGGCCTGAGC GCCGCGGGGC 650

25 AGCTCGCCCC GCCTCCTCCC GCTGGGTTCC GTCTCTCCTT CCGCTTCTTT 700

30 GTCTTTCTCT GCCGCTGTCG GTGTCTGTCT GTCTGCTCTT AGCTGTCTCC 750

ATTGCCTCGG CCTTCTTTGC TTTTGTGGG GGAGAGGGGA GGGGACGGGC 800

35 AGGGTCTCTG TCGCCCAGGC TGGGGTGCAG TGGCGCGATC CCAGCACTGC 850

AGCCTCAACC TCCTGGGCTC AAGCCATCCT TCCGCCTCAG CTTCCCCAGC 900

40 AGCTGGGACT ACAGGCACGC GCCACCACAG CCGGCTAATT TTTTATTAA 950

45 TTTTTTGTAG AGACGAGGTT TCGCCATGTT GCCCAGGCTG GTCTTGAAC 1000

CCGGGGCTCA AGCGATCC 1018

50

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1018 bases

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CACTTCCCTC GGCCCTAGTC GGTCCCCGGT CGTACTCGGC CTCCCTCCCT 50
10 TCAGACCTTC TGGGGGTCTG ACTAAGGAGT CAGAGTGAAG AAGGGGTGAA 100
CCTCCGGTTC TAGGCAGTCT GTGTGTCGGA ACGCGTGGAG GAGTGGTTTA 150
15 TCGGACTCGT CGACGAGGTC CTTATACACG TCGAGGTCCC TCTGGGGAAG 200
CCCGACGGGT CGAAGAGCGG CGGCGCCGAC GGCCACCGGC CGGACTCGCG 250
GGGCCGAGGC TCGGTGCGCC CCGACGGTCA CGTGCTCGCC GACGCCGACC 300
25 TGCGCCGCCG CGACCGGCGC GACGGGGGCG ACGACCTGCG TCACACAGCG 350
GCGGTCCGGC TCGACTTGGG CGCGCGCGGC GCGGACGACG CGGCGGACCT 400
CCTGCGCCGC GCGGTCCGGG CCCGGGACCC GCGGCGGCAC CTCCGGAACG 450
35 ACCGGCGCGA CCCGCGGCGG TTGGCGCCCG GGGCCCGGCT CGGGGGGCGG 500
CGGTGGCGGA GTCGGCGGAG GCGGTGGCCC CAGAAGGGGC GGTTCACGA 550
40 CCCCAGAGCG CAAACGCCGG AGATGGCGCT CACCGACTCG GCGTGGCTCC 600
CGCTGGACCC GGTCGACGAC GGGCCCCCGA GCCGGACTCG CGGCGCCCCG 650
45 TCGAGCGGGG CGGAGGAGGG CGACCCAAGG CAGAGAGGAA GCGAAGAAA 700
CAGAAAGAGA CGGCGACAGC CACAGACAGA CAGACGAGAA TCGACAGAGG 750
TAACGGAGCC GGAAGAAACG AAAAACACCC CCTCTCCCCT CCCCTGCCCC 800

TCCCAGAGAC AGCGGGTCCG ACCCCACGTC ACCGCGCTAG GGTCGTGACG 850

TCGGAGTTGG AGGACCCGAG TTCGGTAGGA AGGCGGAGTC GAAGGGGTCG 900

TCGACCCTGA TGTCCGTGCG CGGTGGTGTC GGCCGATTAA AAAATAAATT 950

AAAAAACATC TCTGCTCCAA AGCGGTACAA CGGGTCCGAC CAGAACTTGA 1000

GGCCCCGAGT TCGCTAGG 1018

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ser	Arg	Arg	Glu	Gly	Ser	Leu	Glu	Asp	Pro	Gln	Thr	Asp	Ser	
1				5				10						15	
Ser	Val	Ser	Leu	Leu	Pro	His	Leu	Glu	Ala	Lys	Ile	Arg	Gln	Thr	
			20					25						30	
His	Ser	Leu	Ala	His	Leu	Leu	Thr	Lys	Tyr	Ala	Glu	Gln	Leu	Leu	
			35					40						45	
Gln	Glu	Tyr	Val	Gln	Leu	Gln	Gly	Asp	Pro	Phe	Gly	Leu	Pro	Ser	
			50					55						60	
Phe	Ser	Pro	Pro	Arg	Leu	Pro	Val	Ala	Gly	Leu	Ser	Ala	Pro	Ala	
			65					70						75	
Pro	Ser	His	Ala	Gly	Leu	Pro	Val	His	Glu	Arg	Leu	Arg	Leu	Asp	
			80					85						90	
Ala	Ala	Ala	Leu	Ala	Ala	Leu	Pro	Pro	Leu	Leu	Asp	Ala	Val	Cys	
			95					100						105	
Arg	Arg	Gln	Ala	Glu	Leu	Asn	Pro	Arg	Ala	Pro	Arg	Leu	Leu	Arg	
			110					115						120	
Arg	Leu	Glu	Asp	Ala	Ala	Arg	Gln	Ala	Arg	Ala	Leu	Gly	Ala	Ala	
			125					130						135	
Val	Glu	Ala	Leu	Leu	Ala	Ala	Leu	Gly	Ala	Ala	Asn	Arg	Gly	Pro	
			140					145						150	

Arg Ala Glu Pro Pro Ala Ala Thr Ala Ser Ala Ala Ser Ala Thr
 155 160 165

5 Gly Val Phe Pro Ala Lys Val Leu Gly Leu Arg Val Cys Gly Leu
 170 175 180

Tyr Arg Glu Trp Leu Ser Arg Thr Glu Gly Asp Leu Gly Gln Leu
 185 190 195

10 Leu Pro Gly Gly Ser Ala
 200 201

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